

(1) GENERAL INFORMATION:

(i) \ APPLICANT:

(A) NAME: Yeda Research and Development Co. Ltd.
(B) STREET: Weizmann Institute of Science, P.O.B. 95
(C) CITY: Rehovot
(D) COUNTRY: Israel
(E) POSTAL CODE (ZIP): 76100
(F) TELEPHONE: 972-8-9344093
(G) TELEFAX: 972-8-9470739

(A) NAME: REVEL, Michel
(B) STREET: Beit Brazil 5, Weizmann Institute of Science
(C) CITY: Rehovot
(E) COUNTRY: Israel
(F) POSTAL CODE (ZIP): 76100

(A) NAME: CHEBATH, Judith
(B) STREET: Rehov Miller 13
(C) CITY: Renovot
(E) COUNTRY: Israel
(F) POSTAL CODE (ZIP): 76284

(A) NAME: LAPIDOT, Tsvee
(B) STREET: Rehov Boxer 6
(C) CITY: Ness-Ziona
(E) COUNTRY: Israel
(F) POSTAL CODE (ZIP): 74046

(A) NAME: KOLLET, Orit
(B) STREET: Rehov Ramat Chen 14
(C) CITY: Ramat Gan
(E) COUNTRY: Israel
(F) POSTAL CODE (ZIP): 52232

(ii) TITLE OF INVENTION: Chimeric Interleukin-6 Soluble Receptor/Ligand Protein, Analogs thereof and Uses thereof

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 121284
(B) FILING DATE: 10-JUL-1997

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: IL 122818
(B) FILING DATE: 30-DEC-1997

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

Glu Phe Gly Ala Gly Leu Val Leu Gly Gly Gln Phe Met
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

00462416-041300

50

20

25

30

Gly	Val	Leu	Thr	Ser	Leu	Pro	Gly	Asp	Ser	Val	Thr	Leu	Thr	Cys	Pro
		35					40					45			
Gly	Val	Glu	Pro	Glu	Asp	Asn	Ala	Thr	Val	His	Trp	Val	Leu	Arg	Lys
		50				55					60				
Pro	Ala	Ala	Gly	Ser	His	Pro	Ser	Arg	Trp	Ala	Gly	Met	Gly	Arg	Arg
65					70					75					80
Leu	Leu	Leu	Arg	Ser	Val	Gln	Leu	His	Asp	Ser	Gly	Asn	Tyr	Ser	Cys
				85					90					95	
Tyr	Arg	Ala	Gly	Arg	Pro	Ala	Gly	Thr	Val	His	Leu	Leu	Val	Asp	Val
			100					105						110	
Pro	Pro	Glu	Glu	Pro	Gln	Leu	Ser	Cys	Phe	Arg	Lys	Ser	Pro	Leu	Ser
		115					120					125			
Asn	Val	Val	Cys	Glu	Trp	Gly	Pro	Arg	Ser	Thr	Pro	Ser	Leu	Thr	Thr
		130				135					140				
Lys	Ala	Val	Leu	Leu	Val	Arg	Lys	Phe	Gln	Asn	Ser	Pro	Ala	Glu	Asp
145					150					155					160
Phe	Gln	Glu	Pro	Cys	Gln	Tyr	Ser	Gln	Glu	Ser	Gln	Lys	Phe	Ser	Cys
				165					170					175	
Gln	Leu	Ala	Val	Pro	Glu	Gly	Asp	Ser	Ser	Phe	Tyr	Ile	Val	Ser	Met
			180					185					190		
Cys	Val	Ala	Ser	Ser	Val	Gly	Ser	Lys	Phe	Ser	Lys	Thr	Gln	Thr	Phe
		195					200					205			
Gln	Gly	Cys	Gly	Ile	Leu	Gln	Pro	Asp	Pro	Pro	Ala	Asn	Ile	Thr	Val
	210					215					220				
Thr	Ala	Val	Ala	Arg	Asn	Pro	Arg	Trp	Leu	Ser	Val	Thr	Trp	Gln	Asp
225					230					235					240
Pro	His	Ser	Trp	Asn	Ser	Ser	Phe	Tyr	Arg	Leu	Arg	Phe	Glu	Leu	Arg
				245					250					255	
Tyr	Arg	Ala	Glu	Arg	Ser	Lys	Thr	Phe	Thr	Thr	Trp	Met	Val	Lys	Asp
			260					265					270		
Leu	Gln	His	His	Cys	Val	Ile	His	Asp	Ala	Trp	Ser	Gly	Leu	Arg	His
		275					280					285			
Val	Val	Gln	Leu	Arg	Ala	Gln	Glu	Glu	Phe	Gly	Gln	Gly	Glu	Trp	Ser
		290				295					300				
Glu	Trp	Ser	Pro	Glu	Ala	Met	Gly	Thr	Pro	Trp	Thr	Glu	Ser	Arg	Ser
305					310					315					320
Pro	Pro	Ala	Glu	Asn	Glu	Val	Ser	Thr	Pro	Met	Gln	Ala	Leu	Thr	Thr
				325					330					335	
Asn	Lys	Asp	Asp	Asp	Asn	Ile	Leu	Phe	Arg	Asp	Ser	Ala	Asn	Ala	Thr
				340				345					350		

Ser Leu Pro Val Glu Phe Met Pro Val Pro Pro Gly Glu Asp Ser Lys
 355 360 365
 Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile
 370 375 380
 Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys
 385 390 395 400
 Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu
 405 410 415
 Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys
 420 425 430
 Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr
 435 440 445
 Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe
 450 455 460
 Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val
 465 470 475 480
 Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr
 485 490 495
 Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala
 500 505 510
 Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser
 515 520 525
 Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
 530 535 540

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu
 1 5 10 15
 Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro
 20 25 30
 Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr
 35 40 45

00462416-041300

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asn Lys Ile
 50 55 60
 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
 65 70 75 80
 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala
 85 90 95
 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu
 100 105 110
 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr
 115 120 125
 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln
 130 135 140
 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
 145 150 155 160
 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu
 165 170 175
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His
 180 185 190
 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala
 195 200 205
 Leu Arg Gln Met Gly Gly Gly Gly Asp Pro Gly Gly Gly Gly Gly Gly
 210 215 220
 Pro Gly Val Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser
 225 230 235 240
 Pro Leu Ser Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser
 245 250 255
 Leu Thr Thr Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro
 260 265 270
 Ala Glu Asp Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys
 275 280 285
 Phe Ser Cys Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile
 290 295 300
 Val Ser Met Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr
 305 310 315 320
 Gln Thr Phe Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn
 325 330 335
 Ile Thr Val Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr
 340 345 350
 Trp Gln Asp Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe
 355 360 365
 Glu Leu Arg Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met

005T40" 9T29460

370

375

380

Val Lys Asp Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly
 385 390 395 400

Leu Arg His Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly
 405 410 415

Glu Trp Ser Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu
 420 425 430

Ser Arg Ser Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala
 435 440 445

Leu Thr Thr Asn Lys Asp Asp Asp Asn Ile Leu Phe Arg Asp Ser Ala
 450 455 460

Asn Ala Thr Ser Leu Pro Val
 465 470

00ET40" 9TF429-460